Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1. - 62. (Cancelled)

63. (Currently amended) A fragment complementation system, said system comprising[:] a first oligopeptide sequence and a second oligopeptide sequence;

wherein said first oligopeptide sequence is a fusion protein comprised of and in the direction of translation, ~~comprising~~ an N-terminal fragment of a Class A β-lactamase protein at least 25 amino acids in length, fused through a first break-point terminus to a first flexible polypeptide linker and ~~covalently bonded through the C-terminus of a first Class A β-lactamase protein break-point to~~ a first interactor domain; and

wherein said ~~a~~ second oligopeptide sequence is a fusion protein comprised of and in the direction of translation, a second interactor domain and a second flexible polypeptide linker fused through a second break-point terminus to ~~comprising~~ a C-terminal fragment of a Class A β-lactamase protein at least 25 amino acids in length; ~~covalently bonded through the N-terminus of a second Class A β-lactamase protein break-point to a second interactor domain;~~

wherein said first and second ~~Class A β-lactamase protein~~ break-point termini; ~~and second Class A β-lactamase protein break-point;~~

are within 10 amino acids in either direction from a junction between 2 amino acid residues, wherein said 2 amino acid residues are within a solvent exposed loop between elements of secondary structure and,

wherein upon binding of said first interactor domain with said second interactor domain, said N-terminal fragment and said C-terminal fragment functionally reconstitute to form the Class A β-lactamase protein.

64. (Currently amended) The fragment complementation system of claim 63, wherein said first oligopeptide and said second oligopeptide comprise a signal peptide that translocates said first oligopeptide and said second oligopeptide through the plasma membrane of ~~the~~ a host cell in which said first oligopeptide and said second oligopeptide are expressed.

65. (Canceled)

66. (Currently amended) The fragment complementation system of claim 63, wherein said Class A β-lactamase protein comprises amino acids 26 to 288 of the following sequence:

His	Pro	Glu	Thr	Leu	Val	Lys	Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly				
26				30				35						40					
Ala	Arg	Val	Gly	Tyr	Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu				
				45				50						55					
Glu	Ser	Phe	Arg	Pro	Glu	Glu	Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys				
			60				65						70						
Val	Leu	Leu	Cys	Gly	Ala	Val	Leu	Ser	Arg	Ile	Asp	Ala	Gly	Gln	Glu				
		75				80				85									
Gln	Leu	Gly	Arg	Arg	Ile	His	Tyr	Ser	Gln	Asn	Asp	Leu	Val	Glu	Tyr				
90				95			100							105					
Ser	Pro	Val	Thr	Glu	Lys	His	Leu	Thr	Asp	Gly	Met	Thr	Val	Arg	Glu				
				110			115						120						
Leu	Cys	Ser	Ala	Ala	Ile	Thr	Met	Ser	Asp	Asn	Thr	Ala	Ala	Asn	Leu				
			125				130						135						
Leu	Leu	Thr	Thr	Ile	Gly	Gly	Pro	Lys	Glu	Leu	Thr	Ala	Phe	Leu	His				
		140					145						150						
Asn	Met	Gly	Asp	His	Val	Thr	Arg	Leu	Asp	Arg	Trp	Glu	Pro	Glu	Leu				
	155				160					165									
Asn	Glu	Ala	Ile	Pro	Asn	Asp	Glu	Arg	Asp	Thr	Thr	Met	Pro	Val	Ala				
170				175				180						185					

Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu
190 195 200
Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala
205 210 215
Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp
220 225 230
Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu
235 240 245
Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly
250 255 260 265
Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly
270 275 280
Ala Ser Leu Ile Lys His Trp
285

(SEQ ID NO:2);

wherein said junction is selected from the group consisting of P174 and N175, E197 and L198, K215 and V216, A227 and G228, and G253 and K254.

67. (Canceled).

68. (Previously Presented) The fragment complementation system of claim 63, wherein said fragment complementation system further comprises a first peptide that enhances the functional reconstitution of said N-terminal fragment and said C-terminal fragment in comparison with the identical system without said first peptide, wherein said first peptide is 3-12 amino acids in length.

69. (Previously Presented) The fragment complementation system of claim 68, wherein said first peptide is 3 amino acids in length.

70. (Previously Presented) The fragment complementation system of claim 69, wherein said first peptide is covalently bonded to the active site of a thioredoxin protein, wherein the sequence of said first peptide is GRE.

71. (Currently amended) The fragment complementation system of claim 63, wherein

~~said first oligopeptide further comprises a first polypeptide linker that separates the N-terminal fragment of a Class A β-lactamase protein from the first interactor domain, wherein~~ said first polypeptide linker is 3-30 amino acids in length; and

~~said second oligopeptide further comprises a second polypeptide linker that separates the C-terminal fragment of a Class A β-lactamase protein from the second interactor domain,~~ wherein said second polypeptide linker is 3-30 amino acids in length.

72. (Previously Presented) The fragment complementation system of claim 71, wherein

said first oligopeptide further comprises a first complementation enhancement peptide fused between the N-terminal fragment of a Class A β-lactamase protein and the first polypeptide linker; and

said second oligopeptide further comprises a second complementation enhancement peptide fused between the C-terminal fragment of a Class A β-lactamase protein and the second polypeptide linker

73. (Previously Presented) The fragment complementation system of claim 72, wherein

the sequence of said first complementation enhancement peptide is selected from the group consisting of HSE, GRE, EKR, and NGR, and

the sequence of said second complementation enhancement peptide is selected from the group consisting of REQ, QGN, DGR, GRR and GNS.

74. (Previously Presented) The fragment complementation system of claim 73, wherein

if the sequence of said first complementation enhancement peptide is HSE, then the sequence of said second complementation enhancement peptide is REQ;

if the sequence of said first complementation enhancement peptide is NGR, then the sequence of said second complementation enhancement peptide is selected from the group consisting of REQ and GNS;

if the sequence of said first complementation enhancement peptide is GRE, then the sequence of said second complementation enhancement peptide is DGR; and

if the sequence of said first complementation enhancement peptide is EKR, then the sequence of said second complementation enhancement peptide is GRR.